REMARKS

Applicant conducted a Telephone Interview with the Examiner regarding the submission of Exhibits A and B in response to the Official Action filed on November 16, 2005. The Examiner was unable to read the Exhibits and suggested to divide the Exhibits into 8.5 x 11 pages. Attached is Exhibit B. Please note the Exhibit can be pieced together by referring to the attached grid. Exhibit A is being submitted in a separate transmission in order to prevent the pages of the Exhibits from being intermingled.

By submission of the 8.5 x 11 copies of Exhibit B, applicant respectfully submits that Amendment B is fully responsive to the Official Action dated March 1, 2005. Further, applicant respectfully requests reconsideration of Amendment B.

CONCLUSION

In light of the above amendments and remarks, it is respectfully submitted that the present application is now in proper condition for allowance, and such action is earnestly solicited.

If any small matter should remain outstanding after the Patent Examiner has had an opportunity to review the above Remarks, the Patent Examiner is respectfully requested to telephone the undersigned patent attorney in order to resolve these matters and avoid the issuance of another Official Action.

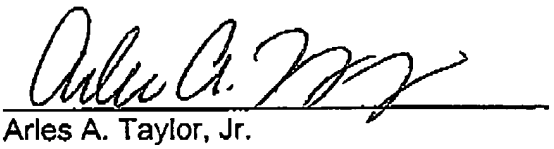
Serial No.: 09/938,714

DEPOSIT ACCOUNT

The Commissioner is hereby authorized to charge any fees associated with the filing of this correspondence to Deposit Account No. **50-0426**.

Respectfully submitted,

JENKINS, WILSON & TAYLOR, P.A.

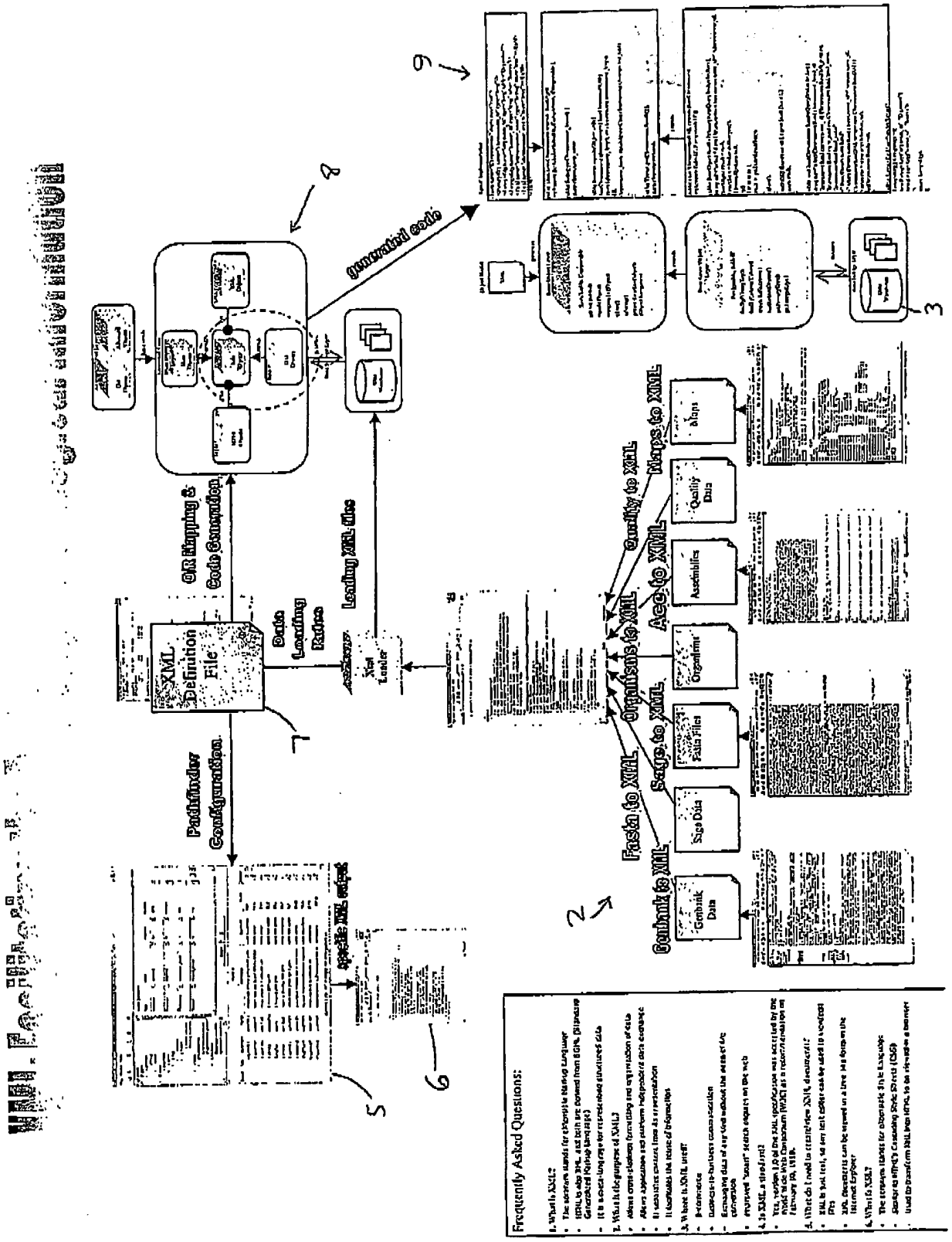
Date: December 15, 2005 By: 

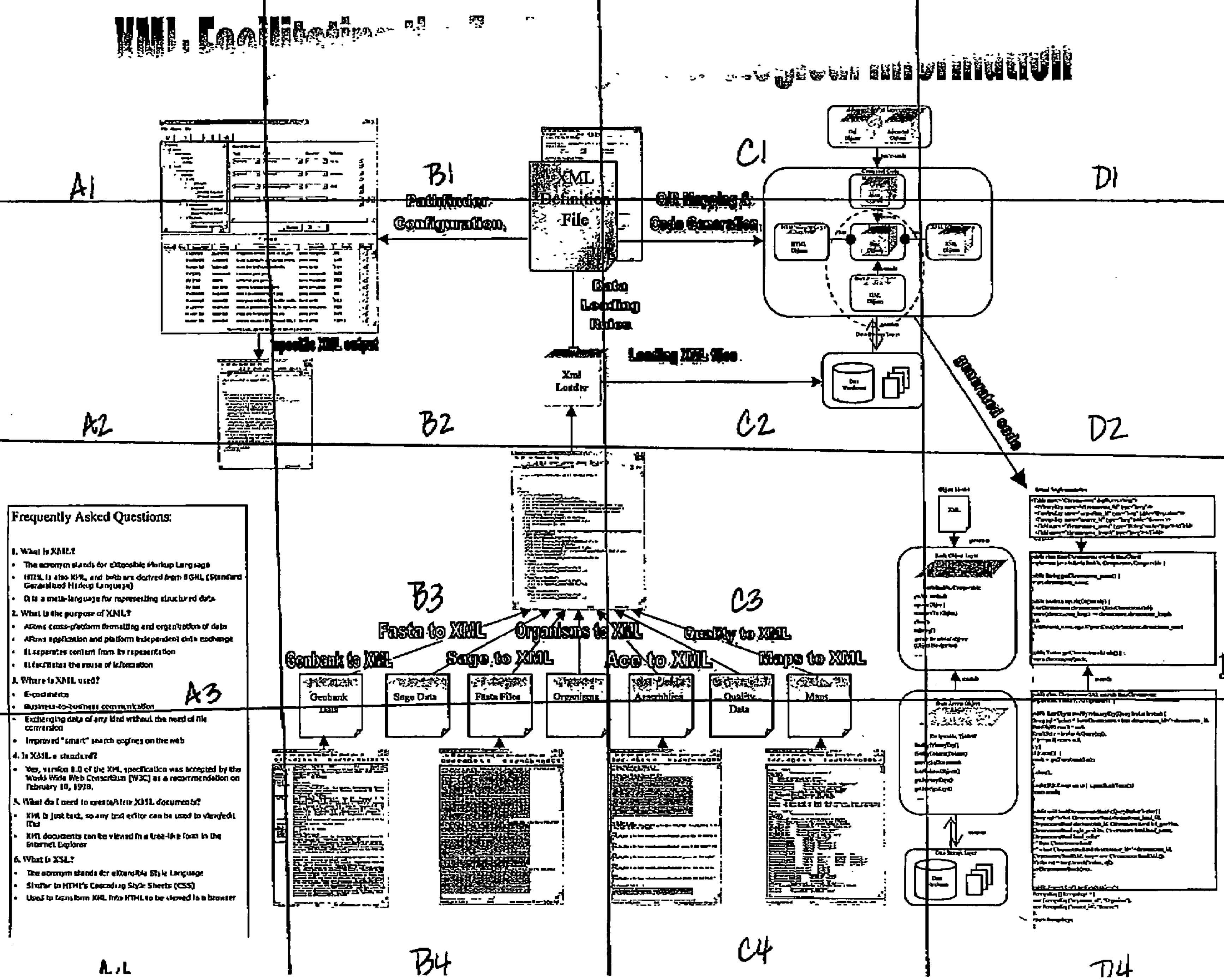
Arles A. Taylor, Jr.
Registration No. 39,395
Customer No. 25297

AAT/BJO/alb

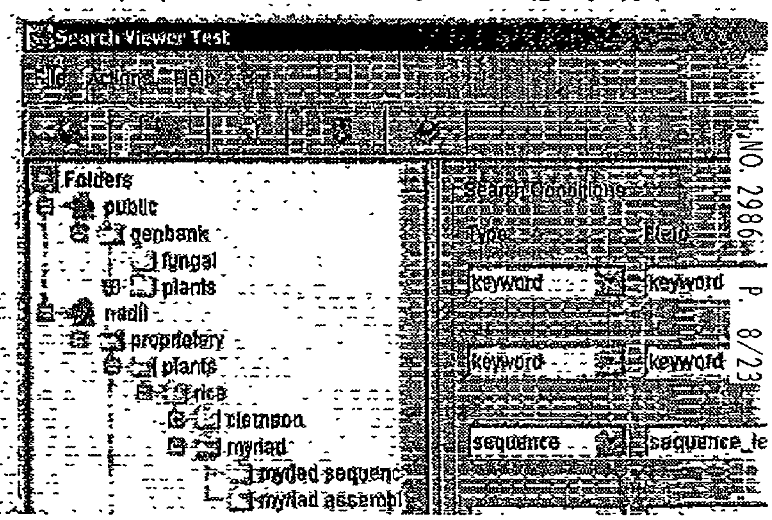
1392/10/22

Exhibit B




A1
A2
A3
A4
B1
B2
B3
B4
C1
C2
C3
C4
D1
D2
D3
D4
XML Definition File
Pathfinder Configuration
O/R Mapping & Code Generation
Data Loading Rules
Loading XML files
Xml Loader
generated code
Genbank to XML
Fasta to XML
Sage to XML
Organisms to XML
Ace to XML
Quality to XML
Maps to XML
Genbank Data
Sage Data
Fasta Files
Organisms
Assemblies
Quality Data
Maps
Frequently Asked Questions:
1. What is XML?
The acronym stands for eXtensible Markup Language
HTML is also XML, and both are derived from SGML (Standard Generalized Markup Language)
It is a meta-language for representing structured data
2. What is the purpose of XML?
Allows cross-platform formatting and organization of data
Allows application and platform independent data exchange
It separates content from its representation
It facilitates the reuse of information
3. Where is XML used?
E-commerce
Business-to-business communication
Exchanging data of any kind without the need of file conversion
Improved "smart" search engines on the web
4. Is XML a standard?
Yes, version 1.0 of the XML specification was accepted by the World Wide Web Consortium (W3C) as a recommendation on February 10, 1998.
5. What do I need to create/view XML documents?
XML is just text, so any text editor can be used to view/edit files
XML documents can be viewed in a tree-like form in the Internet Explorer
6. What is XSL?
The acronym stands for eXtensible Style Language
Similar to HTML's Cascading Style Sheets (CSS)
Used to transform XML into HTML to be viewed in a browser

XML: Facil


Search Viewer Test
Folders
public
genbank
fungal
plants
proprietary
plants
rice
keyword
keyword
keyword
keyword
sequence

A1

- cochliobolus
  - cochliobolus seque…
  - cochliobolus assem…
- fusarium
  - fusarium sequence…
  - fusarium assemblie…

select all

select	Row	accession	name	description
☐	1	aj240902	aaj240902	allagoptera arenaria partial p…
☐	2	ab000595	ab000595	french bean dna for pod stora…
☐	3	ab001386	ab001386	maize dna for fd-v, complete cds
☐	4	x83393	abdnagdha	a.bisporus gdha gene.
☐	5	y12704	abglna	a.bisporus glna gene.
☐	6	y15940	aby15940	agaricus bisporus hypb gene
☐	7	aj240903	aaj240903	attalea allenii partial rps16 ge…
☐	8	ab000125	ab000125	aspergillus nidulans dna for …
☐	9	aj277474	abj277474	agaricus bisporus asl gene f…
☐	10	ab001387	ab001387	maize dna for fd-iii, complete
☐	11	ab001684	ab001684	chlorella vulgaris c-27 chloro…

```
<?xml version="1.0" encoding="UTF-8" ?>
- <!--
    author: Chester Born
    This file was automatically generated
  -->
- <Chromosome chromosome_id="1" source_id="4"
    <chromosome_length>2345</chromosome_le…
    <chromosome_name>Chromosome XYZ</chro…
  - <ChromosomeBand chromosome_id="1">
      <left_position>9.8</left_position>
      <right_position>12.897</right_position>
      <band_name>some band 1</band_name>
    </ChromosomeBand>
  - <ChromosomeBand chromosome_id="1">
      <left_position>55.432</left_position>
      <right_position>23.134</right_position>
      <band_name>some band 2</band_name>
    </ChromosomeBand>
  - <ChromosomeBand chromosome_id="1">
      <left_position>15.123</left_position>
      <right_position>2.123</right_position>
      <band_name>some band 3</band_name>
```

A2

Frequently Asked Questions:

1. What is XML?

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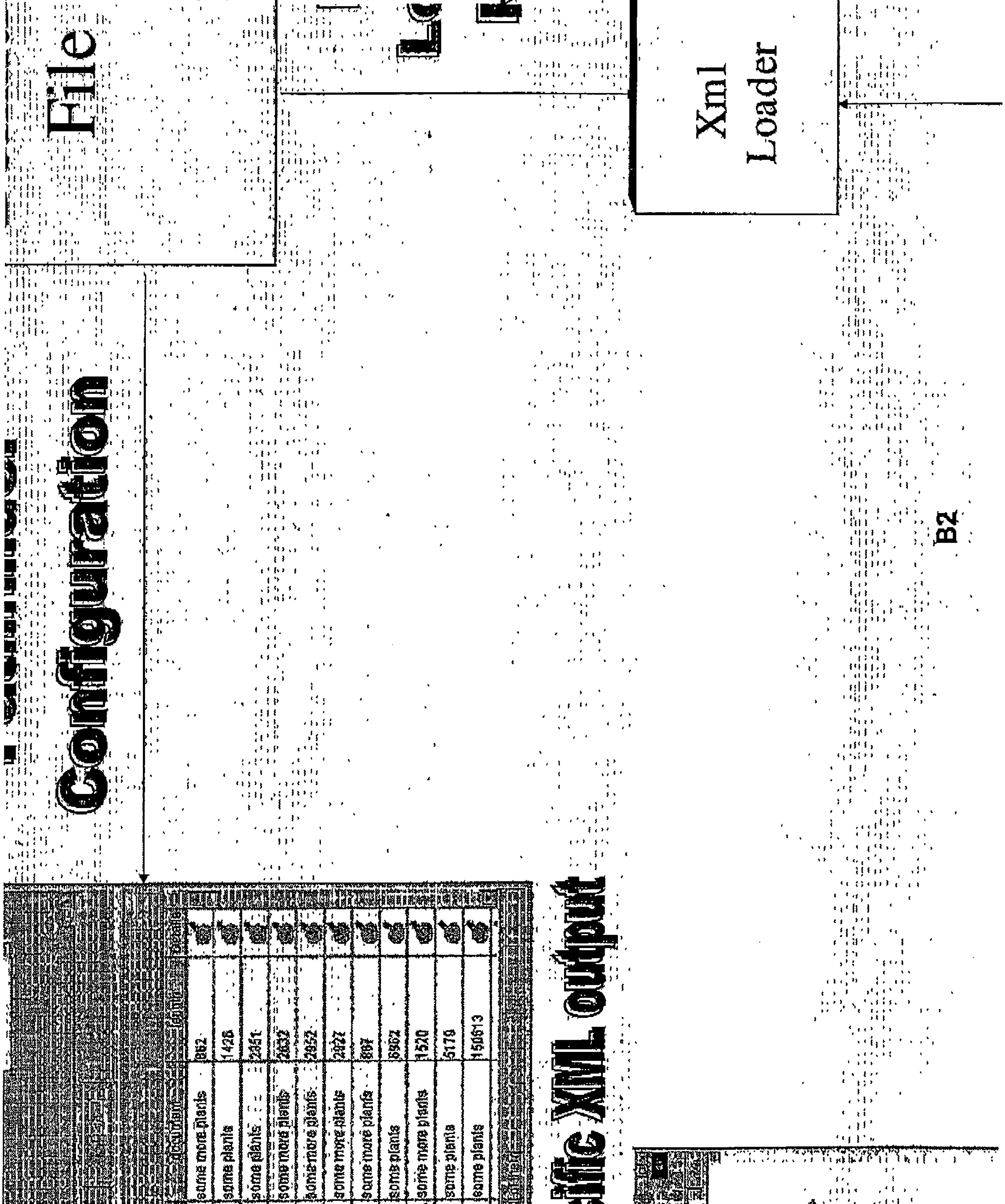
XML


File
Configuration
Xml Loader
XML output
B2

Fasta to XML
Organisms
Sage to XML
Genbank to XML
B3

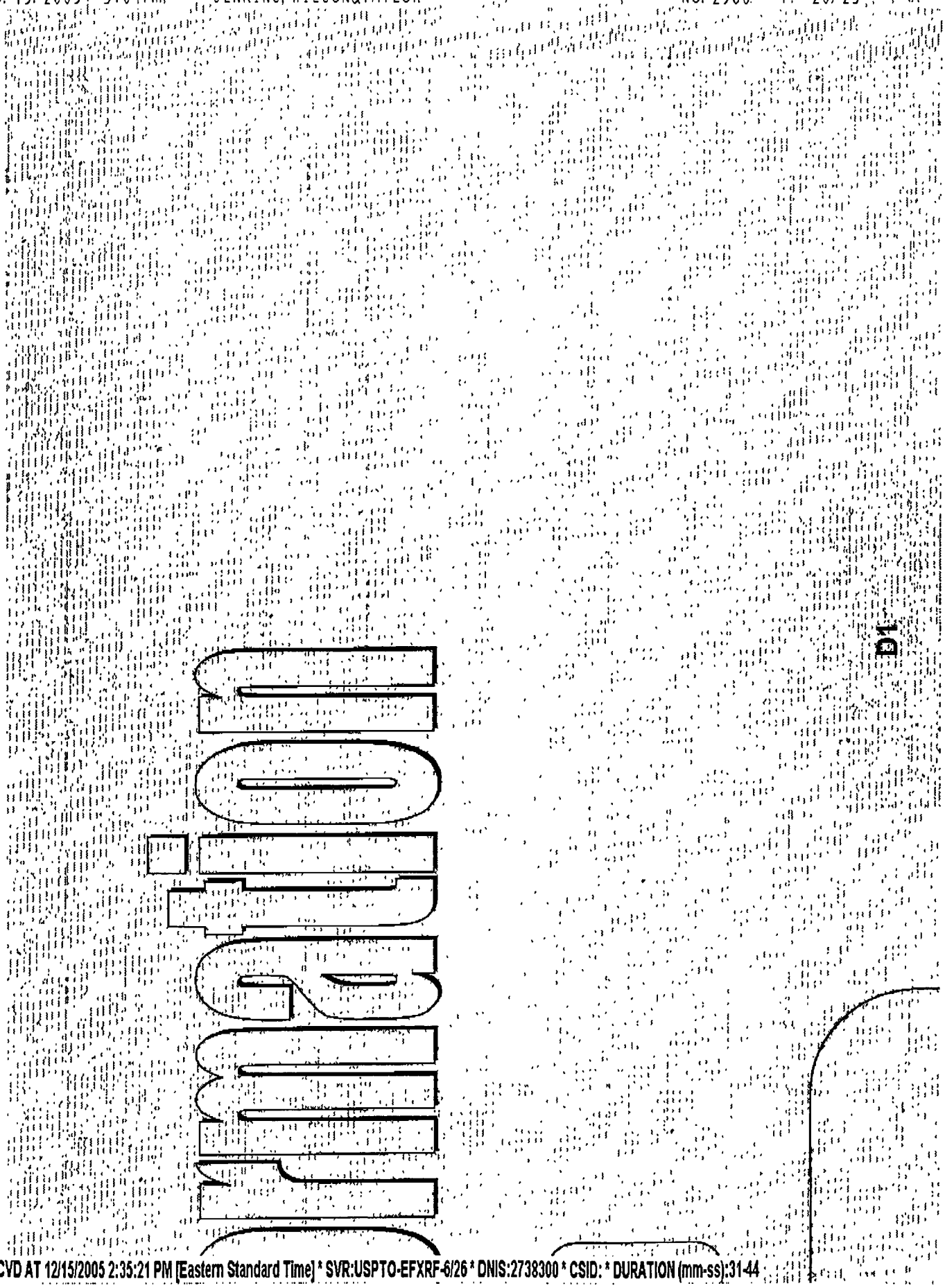
Data
B4

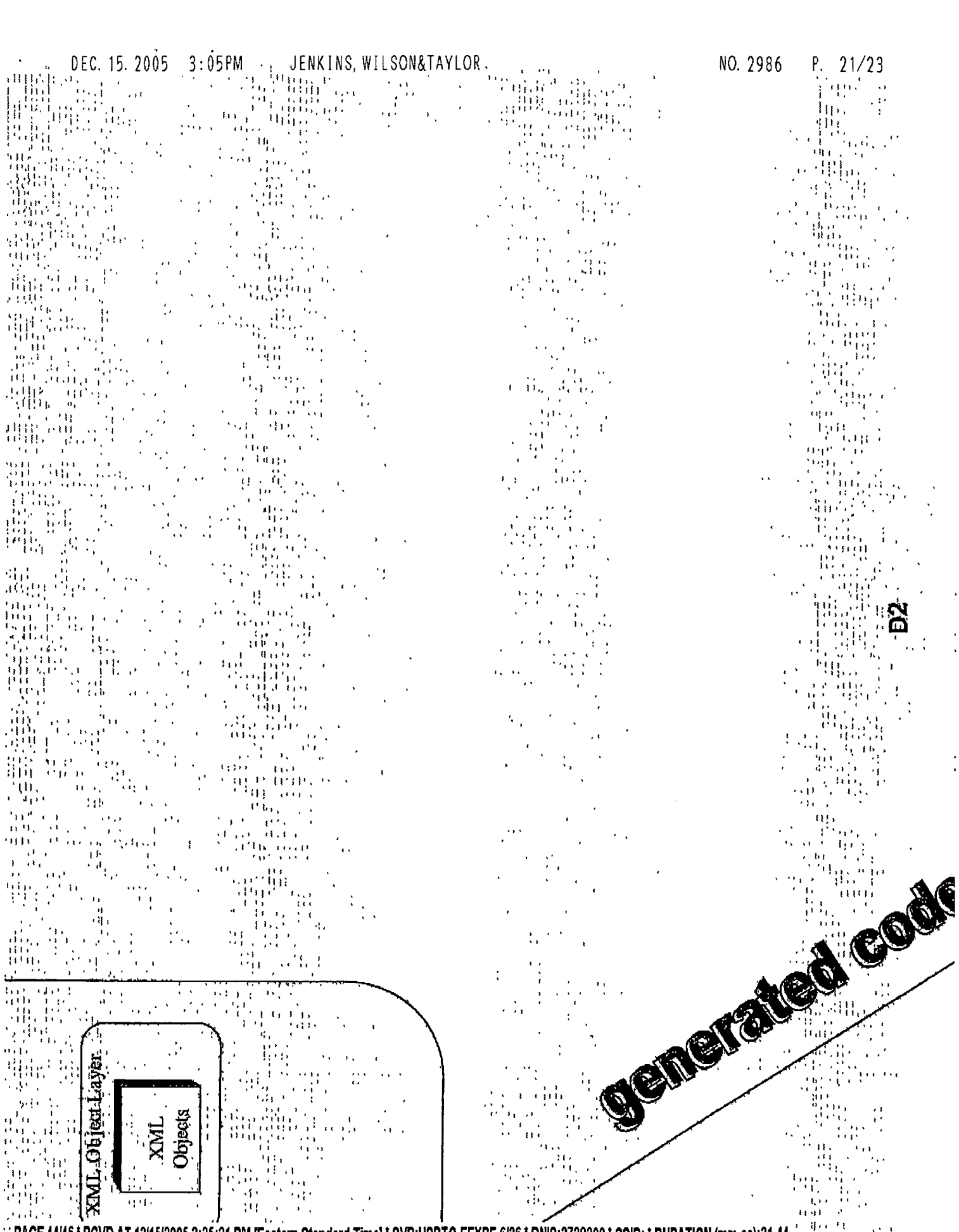
Advanced Object Layer
Gui Objects
Advanced Objects
has/extends
Generated Code
Main Object
Main

Code Generation
Loading XML files
Basic Object Layer
Base Objects
extends
Data Access Layer
DAL Objects
accesses
Data Storage Layer
Data Warehouse
HTML Object Layer
HTML Objects
has

XML
Quality to XML
Maps to XML
Ace to XML
C3

Data
C4


D1


D2
generated code
XML Object Layer
XML Objects

Object Model
XML
generates
Basic Object Layer
ializable, Comparable
thods
ject)
o (Object)
related objects
vigation)
extends
D3
extends
Actual Implementation
<Table name="Chromosome" duplicates="true">
<PrimaryKey name="chromosome_id" type="long" />
<ForeignKey name="organism_id" type="long" table="Organism"/>
<ForeignKey name="source_id" type="long" table="Source"/>
<Field name="chromosome_name" type="String" main="true"></Field>
<Field name="chromosome_length" type="long"></Field>
</Table>
public class BaseChromosome extends BaseObject
implements java.io.Serializable, Comparator, Comparable {
public String getChromosome_name() {
return chromosome_name;
}
public boolean equals(Object obj) {
BaseChromosome chromosome= (BaseChromosome)obj;
return (chromosome_length == chromosome.chromosome_length
&&
chromosome_name.equalsIgnoreCase(chromosome.chromosome_nme)
);
}
public Vector getChromosomeBands() {
return chromosomebands;
}
public class ChromosomeDAL extends BaseChromosome

Data Access Object Layer
Navigatable, TableIF
maryKey()
olumn(Column)
lStatement()
edObjects()
yKeys()
nKeys()
accesses
Data Storage Layer
Data
rehouse
public BaseObject findByPrimaryKey(QueryBroker broker) {
String sql ="select * from Chromosome where chromosome_id='"+chromosome_id;
BaseObject result = null;
ResultSet r = broker.doQuery(sql);
if (r==null) return null;
try{
if (r.next()) {
result = getFromResultSet(r);
}
r.close();
} catch (SQLException x) { x.printStackTrace();}
return result;
}
public void loadChromosomeBands(QueryBroker broker){
String sql="select ChromosomeBand.chromosome_band_id,
ChromosomeBand.chromosome_id, ChromosomeBand.left_position,
ChromosomeBand.right_position, ChromosomeBand.band_name,
ChromosomeBand.band_color"
+" from ChromosomeBand"
+" where ChromosomeBand.chromosome_id='"+chromosome_id;
ChromosomeBandDAL temp= new ChromosomeBandDAL();
Vector res = temp.search(broker, sql);
setChromosomeBands(res);
}
public ForeignKey[] getForeignKeys(){
ForeignKey[] foreignkeys ={
new ForeignKey("organism_id", "Organism"),
new ForeignKey("source_id", "Source")
};
return foreignkeys;
}

D4